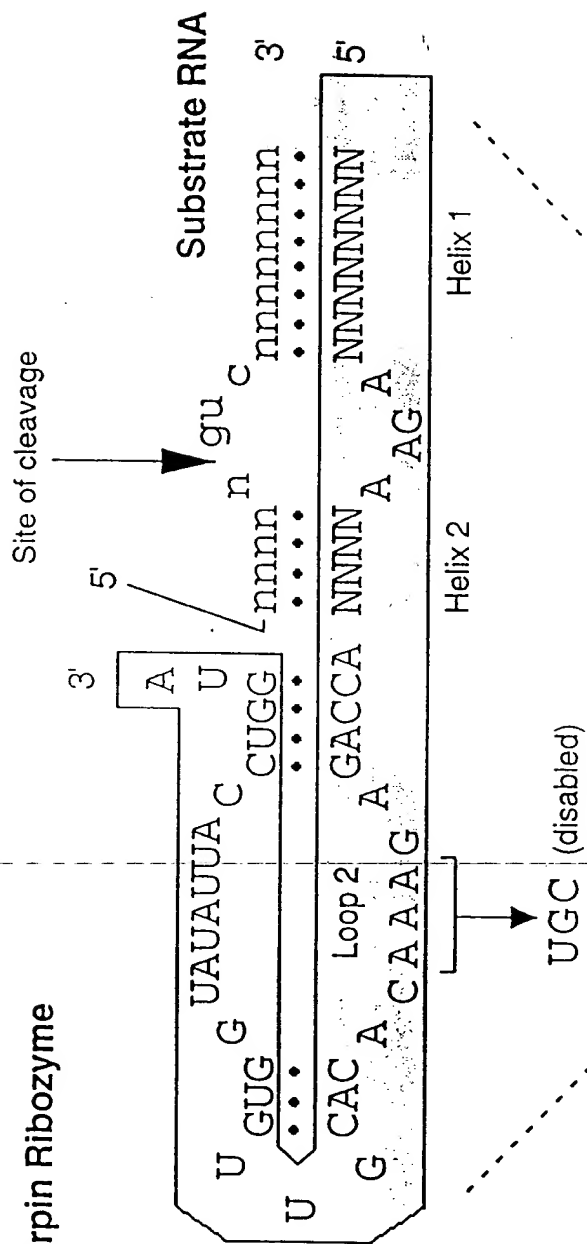
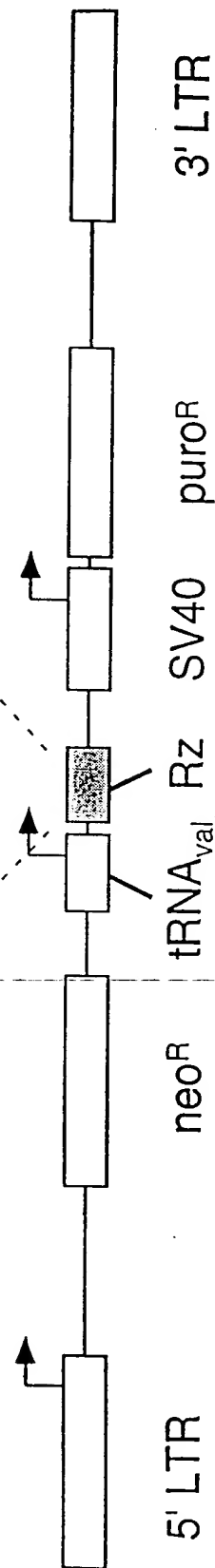


A. Randomized Hairpin Ribozyme



B. Ribozyme Library Vector



Hela

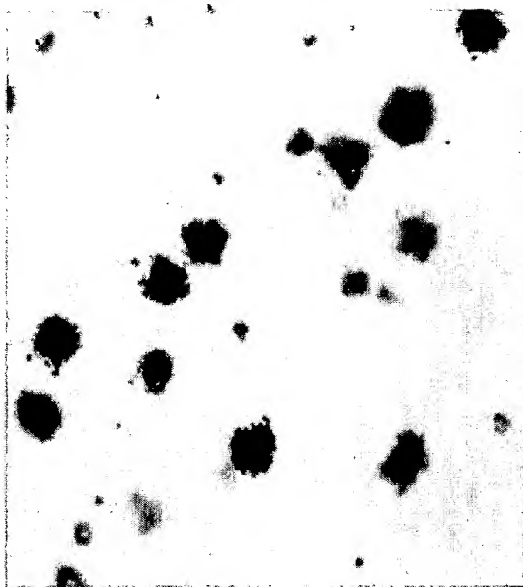


Fig. 2A

HF

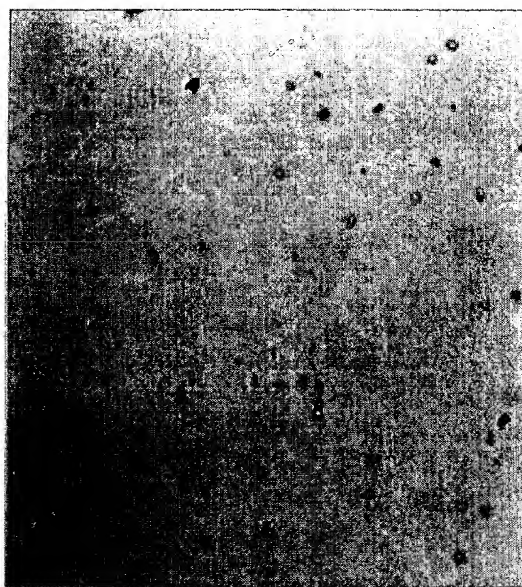


Fig. 2B

HF-568

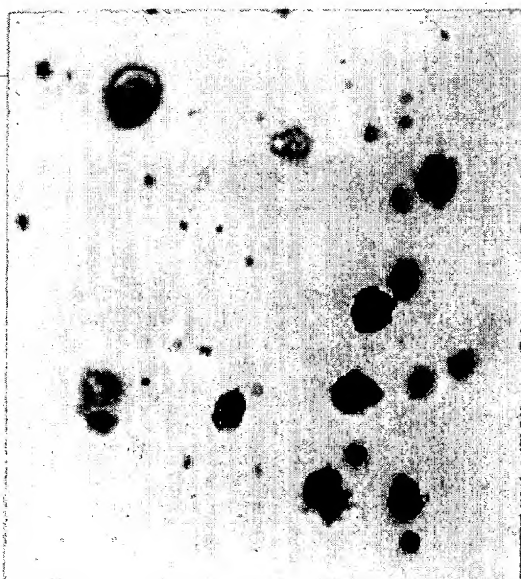


Fig. 2C

HF-d568

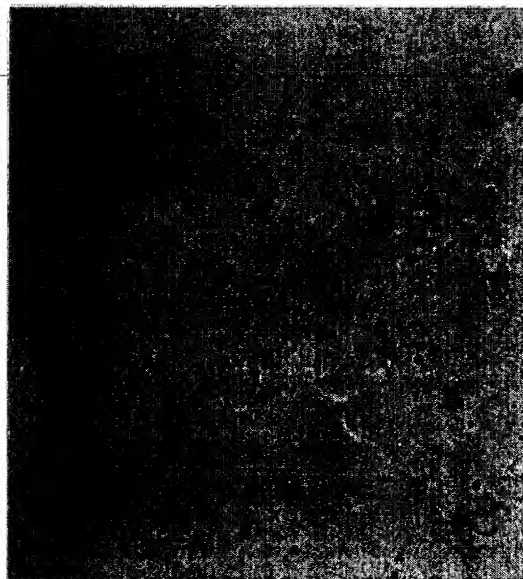
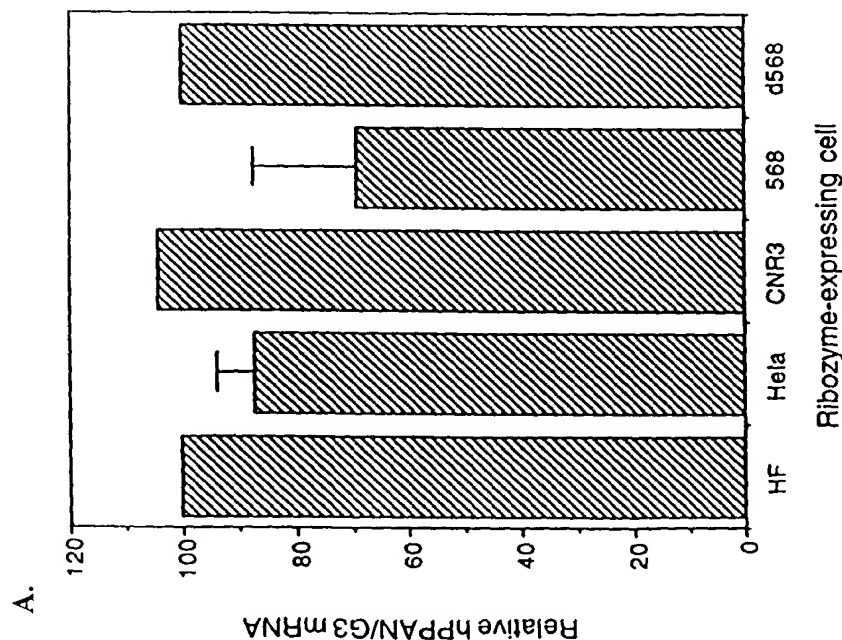
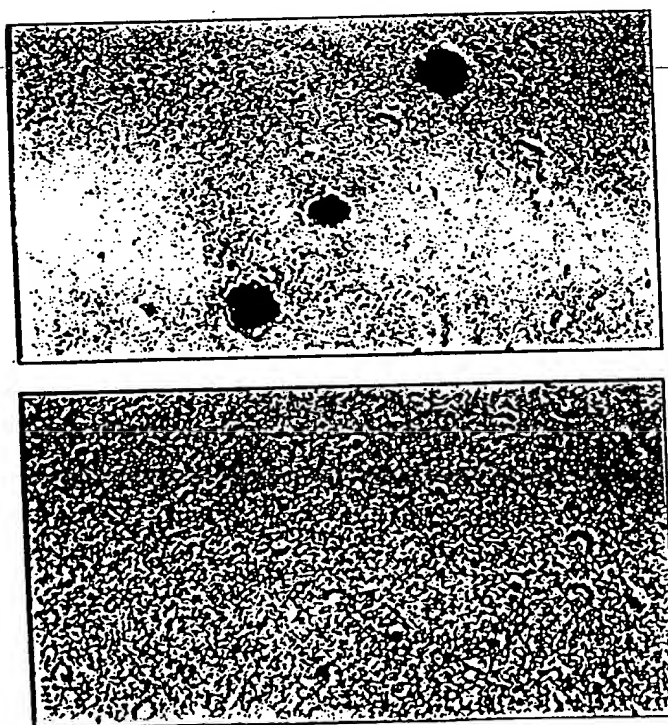
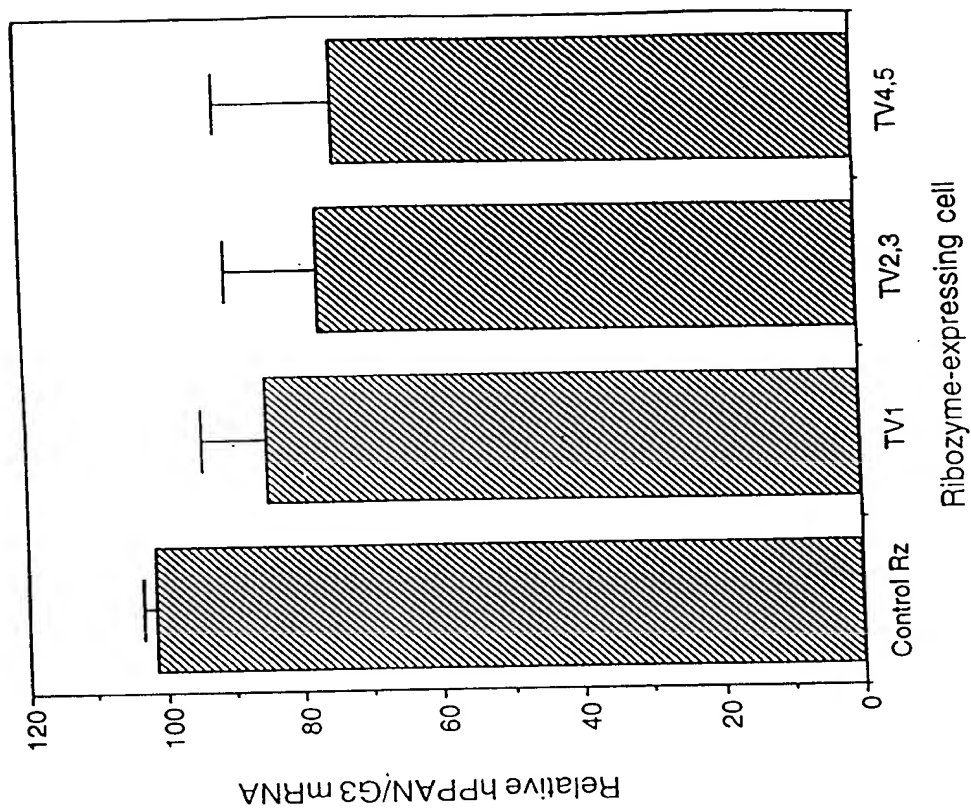


Fig. 2D

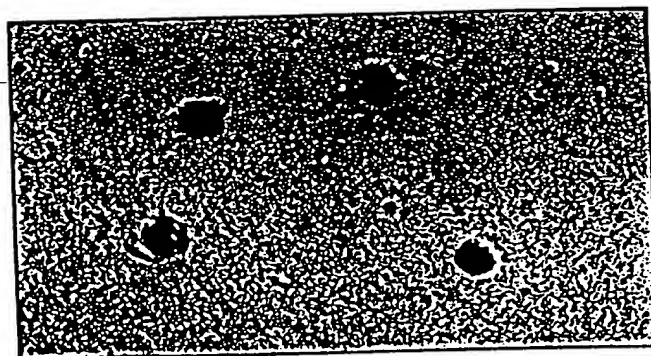
B.

Hs	MGSGSRHQ	KAAPDAOLR	NDAVAMPH	SVFTRCTG	ENFQSLDV	50
Nm	MGSGSRHQ	KNRDAOLR	NDAVAMPH	SVFTRCTG	ENFQSLDV	50
Dm	MG-KKKVP	KRTAFKAS	EPSEIVEAH	SVFTRCTG	ENFQSLDV	49
Hs	RRMEVITAS	RLOVRKNSL	KDCVAVAGPL	SVTHFLIA	QENMEKIM	100
Nm	RRMEVITAS	RLOVRKNSL	KDCVAVAGPL	SVTHFLIA	QENMEKIM	100
Dm	RRMEVITAS	RLOVRKNSL	KDCVAVAGPL	SVTHFLIA	QENMEKIM	99
Hs	RLGGPTLTF	QKKSIVND	VSSIRRRHM	FEQQAHPPL	LAIASFGHG	150
Nm	RLGGPTLTF	QKKSIVND	VSSIRRRHM	FEQQAHPPL	LAIASFGHG	150
Dm	RLGGPTLTF	QKKSIVND	VSSIRRRHM	FEQQAHPPL	LAIASFGHG	149
Hs	MLKLAATMF	QKKSIVND	VSSIRRRHM	FEQQAHPPL	LAIASFGHG	200
Nm	MLKLAATMF	QKKSIVND	VSSIRRRHM	FEQQAHPPL	LAIASFGHG	200
Dm	MLKLAATMF	QKKSIVND	VSSIRRRHM	FEQQAHPPL	LAIASFGHG	199
Hs	WVNGSRGV	KKLOEKFN	SRLODISEL	LAIVAGGV	EAEDQDHI	250
Nm	WVNGSRGV	KKLOEKFN	SRLODISEL	LAIVAGGV	EAEDQDHI	250
Dm	WVNGSRGV	KKLOEKFN	SRLODISEL	LAIVAGGV	EAEDQDHI	249
Hs	TELPOVAGR	ENPQOOSAV	ELTEIGPRMT	LAIVAGGV	EAEDQDHI	300
Nm	TELPOVAGR	ENPQOOSAV	ELTEIGPRMT	LAIVAGGV	EAEDQDHI	300
Dm	TELPOVAGR	ENPQOOSAV	ELTEIGPRMT	LAIVAGGV	EAEDQDHI	298
Hs	SKTEBELQA	ELAEKELAR	KAQQAQA	QVQKQEQ	EAHRKSLR	350
Nm	SKTEBELQA	ELAEKELAR	KAQQAQA	QVQKQEQ	EAHRKSLR	348
Dm	SKTEBELQA	ELAEKELAR	KAQQAQA	QVQKQEQ	EAHRKSLR	348
Hs	MKRVGSD	EEAS-GTISR	IASLELED	DEQDDILEY	ECANGHIS	399
Nm	MKRVGSD	EEAS-GTISR	IASLELED	DEQDDILEY	ECANGHIS	398
Dm	MKRVGSD	EEAS-GTISR	IASLELED	DEQDDILEY	ECANGHIS	373
Hs	EDAFIAR	KAQQAQA	QVQKQEQ	EAHRKSLR	EAEDQDHI	439
Nm	EDAFIAR	KAQQAQA	QVQKQEQ	EAHRKSLR	EAEDQDHI	437
Dm	EDAFIAR	KAQQAQA	QVQKQEQ	EAHRKSLR	EAEDQDHI	423
Hs	---KDRSOQA	QARFPRGAS	RDQAGRG	PGKRVA	---	473
Dm	---KDRSOQA	QARFPRGAS	RDQAGRG	PGKRVA	---	460

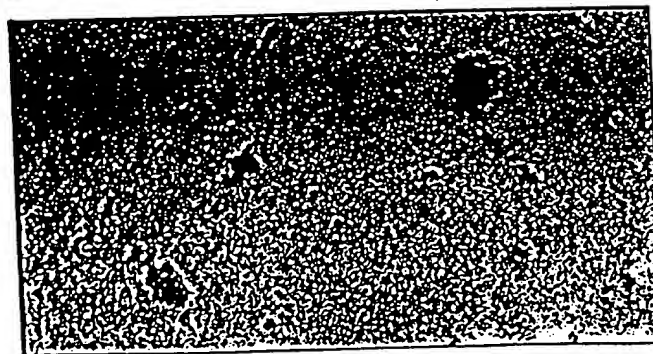




TV1



Control Rz





HF

HeLa

Vector

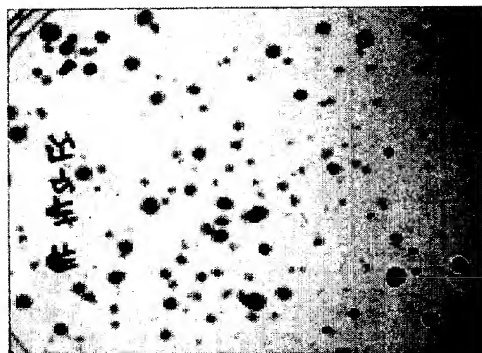


Fig. 5A

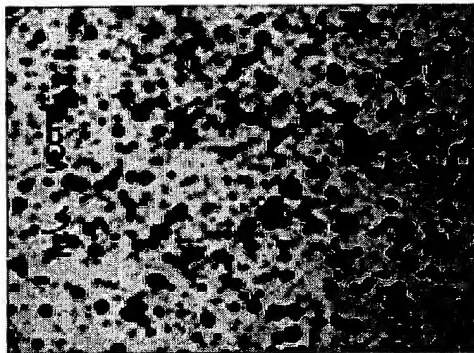


Fig. 5B

hPPAN

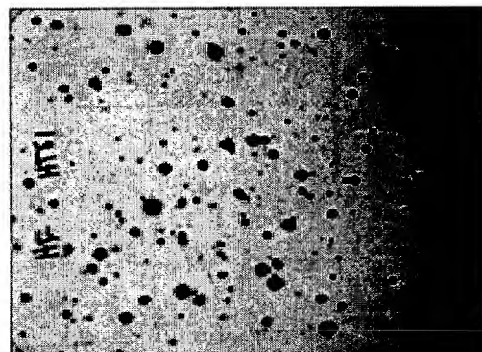


Fig. 5C

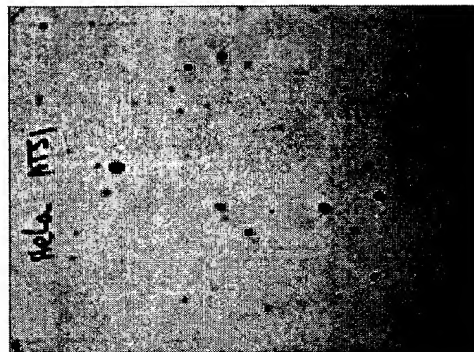


Fig. 5D

FS

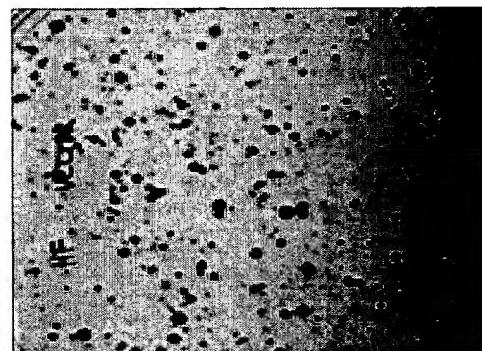


Fig. 5E

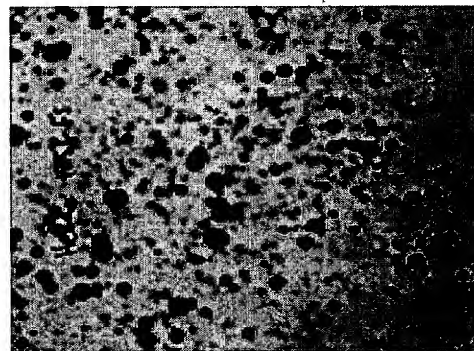


Fig. 5F

	10	20	30	40	50	60
1	GCCTGATGTC	GTCCACGCCC	GTGCCGGCTC	TCAGGCGCCG	GAAGTGAGCT	GCGCACGGCC 60
61	GGAAGCGGCG	GACGCAGGAG	GCCTCGTGGA	GGACACAGCA	GCATGGGACA	GTCAGGGAGG 120
121	TCCCGGCACC	AGAAGCGCGC	CCCGCCCCAG	GCGCAGCTCC	GCAACCTCGA	GGCCTATGCC 180
181	GCGAACCOCG	ACTCGTTTCG	GTTTCACGCGA	GGCTGCACGG	GTCCCAACAT	CCGGCAGCTC 240
241	AGCCTGGACG	TGCGCGCGGT	CATGGAGCCC	GTCAC TGCCA	GCGCTCTGCA	GGTTTCGTAA 300
301	AAGAACTCGC	TGAAGGACTG	CGTGGCAGTG	GCTGGGCCCC	TCGGGCTCAC	ACACTTTCTG 360
361	ATCCTAGCAA	AACAAGAGAC	CAATGTCTAC	TTTAAGCTGA	TGCGCCTCCC	AGGAGGGCCC 420
421	ACCTTGACCT	TCCAGGTCAA	GAAGTACTCG	CTGGTGCCTG	ATGTGGTCTC	CTCACTGCGC 480
481	CGGCACCGCA	TGCACGAGCA	GCAGTTTGCC	CACCCACCCC	TCCTGGTACT	CAACAGCTTT 540
541	GGCCCCCATG	GTATGCATGT	GAAGCTCATG	GCCACCATGT	TCCAGAACCT	GTTCCCTCTC 600
601	ATCAACGTGC	ACAAGGTGAA	CCTGAACACC	ATCAAGCGCT	GCCTCCTCAT	CGACTACAAC 660
661	CCCGACTCCC	AGGAGCTGGA	CTTCGGCCAC	TATAGCATCA	AAGTTGTTCC	TGTGGGCGCG 720
721	AGTCGCGGGA	TGAAGAAGCT	GCTCCAGGAG	AAGTTCCCCA	ACATGAGCCG	CCTGCAGGAC 780
781	ATCAGCGAGC	TGCTGGCCAC	GGGCGCGGGG	CTGTCCGAGA	GCGAGGCAGA	GCCTGACGGC 840
841	GACCACAACA	TCACAGAGCT	GCCTCAGGCT	GTGCTGGGCC	GTGGCAACAT	GCGGGCCCCAG 900
901	CAGAGTGCAG	TGCGGCTCAC	CGAGATCGGC	CCGCGGATGA	CAC TGCAGCT	CATCAAGGTC 960
961	CAGGAGGGCG	TCGGGGAGGG	CAAAGTGATG	TTCCACAGTT	TTGTGAGCAA	GACGGAGGAG 1020
1021	GAGCTGCAGG	CCATCCTGGA	AGCCAAGGAG	AAGAAGCTGC	GGCTGAAGGC	TCAGAGGCAG 1080
1081	GCCCAGCAGG	CCCAGAATGT	GCAGCGCAAG	CAGGAGCAGC	GGGAGGCCCA	CAGAAAGGAG 1140
1141	AGCCTGGAGG	GCATGAAGAA	GGCACGGGTC	GGGGGTAGTG	ATGAAGAGGC	CTCTGGGATC 1200
1201	CTTTCAAGGA	CGGCGAGCCT	GGAGTTGGGT	GAGGACGATG	ATGAACAGGA	AGATGATGAC 1260
1261	ATCAGATATT	TCTGCCAGGC	GGTGGGCGAG	GCGCCCACTG	AGGACCTGTT	CCCGGAGGCC 1320
1321	AAGCAGAAAC	GGCTTGCCAA	GTCTCCAGGG	CGGAAGCGGA	AGCGGTGGGA	AATGGATCGA 1380
1381	GGCAGGGGTC	GCCTTGTGTA	CCAGAAGTTT	CCCAAGACCA	AGGACAAGTC	CCAGGGAGCC 1440
1441	CAGGCCAGGC	GGGGGCCCCAG	AGGGGCTTCC	CGGGATGGTG	GGCGAGGCCG	GGGCCGAGGC 1500
1501	CGCCAGGGGA	AGAGAGTGGC	CTGAGCCCCA	GCCGCACCGG	AGCAGCGGCT	GGATTGAACG 1560
1561	CCCCAGATTG	GGGCCCCAGA	TGTGGCCCTC	GGTTTCCTTT	CATAAAGGAG	TTGTGTCCCC 1620
1621	AGCCCTTCCA	CTCCAGTAAA	GAAGTGAATT	GGCAAAAAAA	AAAA	1664
	10	20	30	40	50	60

		10		20		30		40		50		60	
1		MGQSGRSRHQ		KRAPFQAQLR		NLEAYAANPH		SFVFTRGCTG		RNIRQLSLDV		RRVMEPVTAS 60	
61		RLQVRKKNSL		KDCVAVAGPL		GVTHFLILAK		QETNVYFKLM		RLPGGPTLTF		QVKKYSLVRD 120	
121		VVSSLRRHRM		HEQQFAHPPL		LVLNSFGPHG		MHVKLMATMF		QNLFPSINVH		KVNLNTIKRC 180	
181		LLIDYNPDSQ		ELDFRHYSIK		VVPVGASRGM		KKLLQEKFPN		MSRLQDISEL		LATGAGLSES 240	
241		EAEPDGDHNI		TELPQAVAGR		GNMRAQQSAV		RLTEIGPRMT		LQLIKVQEGV		GEGKVMFHSF 300	
301		VSKTEEELQA		ILEAKEKKLR		LKAQRQAQQA		QNVQRKQEQR		EAHRKKKSLE		MKKARVGGSD 360	
361		EEASGIPSR		ASLELGEDDD		EQEDDDIEYF		CQAVGEAPSE		DLFPEAKQKR		LAKSPGRKRK 420	
421		RWEMDRGRGR		LCDQKFPKTK		DKSQGAQARR		GPRGASRDGG		RGRGRGRPGK		RVAZ 474	
			10		20		30		40		50		60

MM FGQGGKQAAWGSPGGPDIRSAIAPGELRNLESYAAQPHSPV 41
HS

MM FTIG---RAGRNVRQLSLDVRVMEPLTATRLQVRKKNSLKDCVAVAGPLGVTHFLILT 98
HS LGPRVTHTFLILS 13

MM TD--NSVYLKLMRLPGGPTLTFQISKYTLIRDVVSLSRRH-RMHEQQFNHPPLVLVNSFG 155
HS TE--INVYKLMRLPGGPTLTFQVKKYSLVRODVVSLSRRH-RMHEQQFAHPPLVLVNSFG 70

MM PQG-----MHIKLMATMFQNLFPSINVHIVNLNTIKRCLLINYND-SQELDFRHY 205
HS PHG-----MHVVKLMATMFQNLFPSINVHKNLNTIKRCSSXDLKPGFPRSLDFRPI 121

MM SVKVVVPGASRGMKKLLQ-----EKFPNMSRLQDISSELLATGVG----- 244
HS IAFKGGSCWAPNSGGL 137

MM -----LSDSEVEPDGEHN-----TTELPAVAG-RGNMQAQQSA 277

MM VRLTEIGPRMTLQLIKIQEGVGNVNLFSFVHKTEELQAIIAAKEKRLRLKAQRQQA 337

MM AENLQRXRSCRXPTRRRAWQA----- 358

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